IN THE CLAIMS:

Please amend the claims as follows:

1. (Currently amended) A method of ~~analysing~~ analyzing the methylation state of one or more nucleotide sequences comprising the steps of:

a) selecting one or more genomic test nucleotide sequences from one or more subjects that exhibit a phenotype of interest, and one or more corresponding genomic control sequences from one or more control subjects that lack the phenotype of interest;

b) digesting the genomic test nucleotide sequences and ~~the~~ separately digesting genomic control sequences with one or more methylation-sensitive restriction endonucleases that cut unmethylated sequences but not methylated sequences, to produce ends that can be ligated to an adaptor nucleotide sequence;

c) ligating adaptor nucleotide sequences to the ends produced from step b) to produce ligated sequences;

d) cleaving the ligated sequences with one or more methylation-specific endonucleases that cut methylated sequences but not unmethylated sequences, to produce amplifiable test nucleotide sequences, non-amplifiable nucleotide sequences, amplifiable control nucleotides sequences and non-amplifiable control nucleotide sequences;

e) amplifying the amplifiable test nucleotide sequences and amplifiable control nucleotide sequences to produce amplified test nucleotide sequences and amplified control nucleotide sequences;

f) ~~labelling~~ labeling the amplified test nucleotide sequences from step e) with a first label, and ~~labelling~~ labeling the amplified control nucleotide sequence from step e) with a second label;

g) ~~hybridising~~ hybridizing the ~~labelled~~ labeled products of ~~stepf)~~ step f) with an array comprising a series of nucleotide sequences that are capable of ~~hybridising~~ hybridizing thereto; and

h) determining the ratio of the signals emitted by the first label relative to the second label for each ~~hybridised~~ hybridized nucleotide sequence on the array.

2. (Currently amended) The method of claim 1, further comprising a step of correcting for the effect of DNA sequence variation:

i) amplifying the genomic test nucleotide sequences and separately amplifying the genomic control sequences with a DNA polymerase to produce an unmethylated copy of the genomic test nucleotide sequences and an unmethylated copy of the genomic control sequences;

ii) treating the unmethylated copy of the genomic test nucleotide sequences and separately treating the unmethylated copy of the genomic control sequences with restriction endonuclease digestion, adaptor ligation, amplification, ~~labelling~~ labeling, array ~~hybridisation~~ hybridization, and ratio determination steps that are equivalent to corresponding steps b), c) and e-h); and

iii) comparing the one or more ratios determined in step ~~i~~ ii) to the one or more ratios determined in step h).

3. (Canceled)

4. (Currently amended) The method of claim 1, wherein the ~~CpG~~ methylation specific endonuclease is McrBC.

5. (Currently amended) The method of claim 1, wherein the methylation-sensitive restriction endonuclease comprises ~~is a cocktail comprising~~ HpaII, Bsul51 (ClaI), Hin61, AciI (SsiI), TaiI, or any combination thereof.

6. (Currently amended) The method of claim 1, wherein step f) further comprises ~~labelling~~ labeling the non-amplified test nucleotide sequences from step d) with the first label, and ~~labelling~~ labeling the non-amplified control nucleotide sequences from step d) with a second label.

7. (Currently amended) The method of claim 1, wherein the phenotype of interest comprises ~~a disease such as~~ cancer, diabetes, Alzheimer's disease, or schizophrenia, multiple sclerosis, psoriasis, atherosclerosis, asthma, autism, or rheumatoid arthritis.

8. (Currently amended) The method of claim 1, wherein ~~said probe is a~~ the first label, second label or both are chemically reactive ~~fluorophore~~ fluorophores.

9. (Currently amended) The method of claim 1, wherein said chemically reactive ~~fluorophore is~~ fluorophores are independently Cy 3 or Cy 5.

10-19. (Canceled)

20. (Withdrawn, Currently amended) A kit comprising one or more genomic test nucleotide sequences, one or more corresponding genomic control nucleotide sequences, one or more frequent cutting restriction endonucleases, one or more specific adaptor nucleotide sequences, one or more methylation-sensitive restriction endonucleases, one or more CpG specific restriction endonucleases, one or more probes for ~~labelling~~ labeling the nucleotide sequences, one or more microarrays capable ~~hybridising~~ hybridizing to the genomic test and control nucleotide sequences, software for displaying and/or ~~analysing~~ analyzing the sequences ~~labelling~~ labeling to the microarray, reagents and/or enzymes for amplifying nucleotide sequences, or any combination thereof.

21. (Currently amended) A method of identifying DNA sequence variation in a methylation-state-analysis of one or more nucleotide sequences comprising the steps of:

a) selecting one or more genomic test nucleotide sequence from one or more subjects that exhibit a disease phenotype of interest~~, for example a disease such as but not limited to cancer, diabetes, Alzheimer's disease, schizophrenia or the like,~~ and one or more corresponding genomic control sequences from one or more control subjects that lack the disease phenotype of interest;

b) amplifying the genomic test nucleotide sequences and separately amplifying the genomic control sequences with a DNA polymerase, ~~for example without limitation a Phi29 DNA polymerase,~~ to produce an unmethylated copy of the genomic test nucleotide sequences and an unmethylated copy of the genomic control sequences;

c) treating the unmethylated copy of the genomic test nucleotide sequences and separately treating the unmethylated copy of the genomic control sequences with restriction endonuclease digestion, adaptor ligation, amplification, ~~labelling~~ labeling, array ~~hybridisation~~ hybridization, and ratio determination steps ~~that are equivalent to corresponding steps in the methylation-state-analysis;~~, and;

d) comparing the one or more ratios determined in step c) to the one or more ratios of the methylation-state-analysis, thereby identifying DNA sequence variation in the methylation-state-analysis.

22. (Canceled)